Untitled

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 19:55:40 ; Search time 9295.23 Seconds
                                            (without alignments)
                                            11313.373 Million cell updates/sec

Title: US-10-031-067A-8
Perfect score: 1850
Sequence: 1 ctcgaggatccagagacggc..........tctgtattaccatacggggg 1850

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size :   0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_in:*
                3: gb_env:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pr:*
                9: gb_ro:*
                10: gb_sts:*
                11: gb_sy:*
                12: gb_un:*
                13: gb_vi:*
                14: gb_htg:*
                15: gb_pl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1850	100.0	1850	6	AX079247	AX079247 Sequence
	2	1850	100.0	1850	6	AX079256	AX079256 Sequence
	3	1243	67.2	2500	8	AF233371	AF233371 Homo sapi
c	4	904	48.9	8913	6	AX598719	AX598719 Sequence
c	5	904	48.9	11913	6	CQ787205	CQ787205 Sequence
c	6	904	48.9	11913	6	CQ806558	CQ806558 Sequence
c	7	904	48.9	11913	6	AX795666	AX795666 Sequence
c	8	904	48.9	11913	6	AX822117	AX822117 Sequence

c	9	904	48.9	11913	6	AX825757	AX825757 Sequence
c	10	904	48.9	50678	8	AY245105	AY245105 Homo sapi
c	11	904	48.9	127580	8	HSDJ74J1	AL049692 Human DNA
c	12	904	48.9	248214	14	AL138811	AL138811 Homo sapi
	13	277	15.0	277	6	AX079248	AX079248 Sequence
	14	216	11.7	738	10	BV606780	BV606780 S216P6146
	15	58	3.1	260	6	BD053613	BD053613 Sequence
	16	58	3.1	260	6	AX918080	AX918080 Sequence
c	17	31	1.7	8144	6	AX251388	AX251388 Sequence
c	18	31	1.7	8913	6	AX598871	AX598871 Sequence
	19	31	1.7	8913	6	AX598872	AX598872 Sequence
c	20	31	1.7	11523	6	AX251395	AX251395 Sequence
	21	31	1.7	11523	6	AX251396	AX251396 Sequence
c	22	31	1.7	11523	6	AX278012	AX278012 Sequence
	23	31	1.7	11523	6	AX278013	AX278013 Sequence
c	24	31	1.7	11523	6	AX323709	AX323709 Sequence
	25	31	1.7	11523	6	AX323710	AX323710 Sequence
c	26	31	1.7	11523	6	AX346824	AX346824 Sequence
	27	31	1.7	11523	6	AX346825	AX346825 Sequence
c	28	31	1.7	11523	6	AX347440	AX347440 Sequence
	29	31	1.7	11523	6	AX347441	AX347441 Sequence
c	30	31	1.7	11523	6	AX349161	AX349161 Sequence
	31	31	1.7	11523	6	AX349162	AX349162 Sequence
c	32	31	1.7	11523	6	AX657802	AX657802 Sequence
	33	31	1.7	11523	6	AX657803	AX657803 Sequence
c	34	31	1.7	11523	6	AX659076	AX659076 Sequence
	35	31	1.7	11523	6	AX659077	AX659077 Sequence
c	36	31	1.7	11913	6	CQ787424	CQ787424 Sequence
	37	31	1.7	11913	6	CQ787425	CQ787425 Sequence
c	38	31	1.7	11913	6	CQ806811	CQ806811 Sequence
	39	31	1.7	11913	6	CQ806812	CQ806812 Sequence
c	40	31	1.7	11913	6	AX795749	AX795749 Sequence
	41	31	1.7	11913	6	AX795750	AX795750 Sequence
c	42	31	1.7	11913	6	AX822257	AX822257 Sequence
	43	31	1.7	11913	6	AX822258	AX822258 Sequence
c	44	31	1.7	11913	6	AX825897	AX825897 Sequence
	45	31	1.7	11913	6	AX825898	AX825898 Sequence

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:08:34 ; Search time 1093.3 Seconds
                                              (without alignments)
                                              11277.487 Million cell updates/sec

Title: US-10-031-067A-8
Perfect score: 1850
Sequence: 1 ctcgaggatccagagacggc..........tctgtattaccatacggggg 1850

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size :   0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_21:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*
                14: geneseqn2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1   1850   100.0   1850 4   AAD02661   Aad02661 Human Wil
c   2   904   48.9   8913 8   ABZ09919   Abz09919 Human 5'
c   3   904   48.9   11913 10   ADB53953   Adb53953 WT1 genom
c   4   904   48.9   11913 13   ADS88992   Ads88992 Human WT1
      5   277   15.0   277 4   AAD02662   Aad02662 Human WT1
      6   58   3.1   260 3   AAC29868   Aac29868 Human sec
c   7   31   1.7   8144 4   AAS46634   Aas46634 Tumour su
c   8   31   1.7   8913 8   ABZ10071   Abz10071 Haematopo
      9   31   1.7   8913 8   ABZ10072   Abz10072 Haematopo
c   10   31   1.7   11523 4   AAS45467   Aas45467 Chemical1

	11	31	1.7	11523	4	AAS45468	Aas45468 Chemical1
c	12	31	1.7	11523	4	AAS46641	Aas46641 Tumour su
	13	31	1.7	11523	4	AAS46642	Aas46642 Tumour su
	14	31	1.7	11523	6	ABL33923	Abl33923 Human imm
c	15	31	1.7	11523	6	ABL33922	Abl33922 Human imm
	16	31	1.7	11523	6	ABK34002	Abk34002 Human DNA
c	17	31	1.7	11523	6	ABK34001	Abk34001 Human DNA
	18	31	1.7	11523	6	ABK28324	Abk28324 DNA trans
c	19	31	1.7	11523	6	ABK28323	Abk28323 DNA trans
	20	31	1.7	11523	8	ADA20383	Ada20383 Prostate
c	21	31	1.7	11523	8	ADA20382	Ada20382 Prostate
c	22	31	1.7	11523	8	ADA84189	Ada84189 Human ren
	23	31	1.7	11523	8	ADA84190	Ada84190 Human ren
	24	31	1.7	11913	10	ADB54094	Adb54094 Pretreate
c	25	31	1.7	11913	10	ADB54093	Adb54093 Pretreate
	26	31	1.7	11913	13	ADS89246	Ads89246 Oligonucl
c	27	31	1.7	11913	13	ADS89245	Ads89245 Oligonucl
	28	24	1.3	8144	4	AAS46633	Aas46633 Tumour su
c	29	23	1.2	8170	6	ABK28257	Abk28257 DNA trans
c	30	23	1.2	8913	8	ABZ10217	Abz10217 Haematopo
c	31	23	1.2	11913	10	ADB54221	Adb54221 Pretreate
c	32	23	1.2	11913	13	ADS89519	Ads89519 Oligonucl
c	33	20	1.1	522	13	ADQ54009	Adq54009 Novel can
	34	20	1.1	540	14	ADY64337	Ady64337 Human NBS
c	35	20	1.1	924	10	ACF69369	Acf69369 Photorhab
c	36	20	1.1	963	6	ABK10139	Abk10139 Z. mobili
	37	20	1.1	50657	13	ABD33455	Abd33455 Murine ca
	38	20	1.1	56495	14	ADW72230	Adw72230 Human Nij
	39	20	1.1	65921	3	AAZ89046	Aaz89046 Human nib
c	40	20	1.1	100779	10	ACF65386_6	Continuation (7 of
	41	20	1.1	110000	10	ACF67367_22	Continuation (23 o
c	42	20	1.1	110000	10	ACF65386_5	Continuation (6 of
c	43	20	1.1	135638	10	ABX34289	Abx34289 S. atrool
c	44	19	1.0	300	3	AAA01052	Aaa01052 Human col
	45	19	1.0	330	4	AAK55787	Aak55787 Human imm

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 21:06:40 ; Search time 363.564 Seconds
                                              (without alignments)
                                              9045.152 Million cell updates/sec

Title: US-10-031-067A-8
Perfect score: 1850
Sequence: 1 ctcgaggatccagagacggc..........tctgtattaccatacggggg 1850

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB ID   Description
----
 c 1   904   48.9   51754 3   US-09-949-016-15009   Sequence 15009, A
 c 2   904   48.9   51754 3   US-09-949-016-15010   Sequence 15010, A
 c 3   904   48.9   51754 3   US-09-949-016-15011   Sequence 15011, A
 c 4   904   48.9   51754 3   US-09-949-016-15012   Sequence 15012, A
 c 5   904   48.9   51754 3   US-09-949-016-15275   Sequence 15275, A
 c 6   904   48.9   51754 3   US-09-949-016-15276   Sequence 15276, A
 c 7   904   48.9   51754 3   US-09-949-016-15277   Sequence 15277, A
 c 8   904   48.9   51754 3   US-09-949-016-15278   Sequence 15278, A
    9   550   29.7   601 3   US-09-949-016-117858   Sequence 117858,
   10   550   29.7   601 3   US-09-949-016-117910   Sequence 117910,
   11   550   29.7   601 3   US-09-949-016-117962   Sequence 117962,
   12   550   29.7   601 3   US-09-949-016-118014   Sequence 118014,
   13   550   29.7   601 3   US-09-949-016-125023   Sequence 125023,
   14   550   29.7   601 3   US-09-949-016-125075   Sequence 125075,
                              Page 1

15	550	29.7	601	3	US-09-949-016-125127	Sequence 125127,
16	550	29.7	601	3	US-09-949-016-125179	Sequence 125179,
17	342	18.5	601	3	US-09-949-016-117857	Sequence 117857,
18	342	18.5	601	3	US-09-949-016-117909	Sequence 117909,
19	342	18.5	601	3	US-09-949-016-117961	Sequence 117961,
20	342	18.5	601	3	US-09-949-016-118013	Sequence 118013,
21	342	18.5	601	3	US-09-949-016-125022	Sequence 125022,
22	342	18.5	601	3	US-09-949-016-125074	Sequence 125074,
23	342	18.5	601	3	US-09-949-016-125126	Sequence 125126,
24	342	18.5	601	3	US-09-949-016-125178	Sequence 125178,
25	293	15.8	601	3	US-09-949-016-117856	Sequence 117856,
26	293	15.8	601	3	US-09-949-016-117908	Sequence 117908,
27	293	15.8	601	3	US-09-949-016-117960	Sequence 117960,
28	293	15.8	601	3	US-09-949-016-118012	Sequence 118012,
29	293	15.8	601	3	US-09-949-016-125021	Sequence 125021,
30	293	15.8	601	3	US-09-949-016-125073	Sequence 125073,
31	293	15.8	601	3	US-09-949-016-125125	Sequence 125125,
32	293	15.8	601	3	US-09-949-016-125177	Sequence 125177,
33	127	6.9	601	3	US-09-949-016-117859	Sequence 117859,
34	127	6.9	601	3	US-09-949-016-117911	Sequence 117911,
35	127	6.9	601	3	US-09-949-016-117963	Sequence 117963,
36	127	6.9	601	3	US-09-949-016-118015	Sequence 118015,
37	127	6.9	601	3	US-09-949-016-125024	Sequence 125024,
38	127	6.9	601	3	US-09-949-016-125076	Sequence 125076,
39	127	6.9	601	3	US-09-949-016-125128	Sequence 125128,
40	127	6.9	601	3	US-09-949-016-125180	Sequence 125180,
41	67	3.6	601	3	US-09-949-016-117855	Sequence 117855,
42	67	3.6	601	3	US-09-949-016-117907	Sequence 117907,
43	67	3.6	601	3	US-09-949-016-117959	Sequence 117959,
44	67	3.6	601	3	US-09-949-016-118011	Sequence 118011,
45	67	3.6	601	3	US-09-949-016-125020	Sequence 125020,

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 21:22:58 ; Search time 1507.31 Seconds
                                             (without alignments)
                                             10149.433 Million cell updates/sec

Title: US-10-031-067A-8
Perfect score: 1850
Sequence: 1 ctcgaggatccagagacggc..........tctgtattaccatacggggg 1850

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size :   0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
                1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	904	48.9	8913	8	US-10-473-126-59	Sequence 59, Appl
c	2	332	17.9	536	4	US-09-925-065A-554005	Sequence 554005,
c	3	110	5.9	896	4	US-09-925-065A-693598	Sequence 693598,
c	4	31	1.7	8144	7	US-10-221-714A-356	Sequence 356, App
c	5	31	1.7	8913	8	US-10-473-126-211	Sequence 211, App
	6	31	1.7	8913	8	US-10-473-126-212	Sequence 212, App
c	7	31	1.7	11523	5	US-10-239-676-175	Sequence 175, App
	8	31	1.7	11523	5	US-10-239-676-176	Sequence 176, App
c	9	31	1.7	11523	5	US-10-172-086-47	Sequence 47, Appl
	10	31	1.7	11523	5	US-10-172-086-48	Sequence 48, Appl
c	11	31	1.7	11523	6	US-10-311-455-1895	Sequence 1895, Ap
	12	31	1.7	11523	6	US-10-311-455-1896	Sequence 1896, Ap
c	13	31	1.7	11523	6	US-10-240-453-197	Sequence 197, App
	14	31	1.7	11523	6	US-10-240-453-198	Sequence 198, App

c	15	31	1.7	11523	7	US-10-221-714A-363	Sequence 363, App
	16	31	1.7	11523	7	US-10-221-714A-364	Sequence 364, App
c	17	31	1.7	11523	7	US-10-311-507-87	Sequence 87, Appl
	18	31	1.7	11523	7	US-10-311-507-88	Sequence 88, Appl
c	19	31	1.7	11523	8	US-10-480-846-47	Sequence 47, Appl
	20	31	1.7	11523	8	US-10-480-846-48	Sequence 48, Appl
	21	24	1.3	8144	7	US-10-221-714A-355	Sequence 355, App
c	22	23	1.2	8170	6	US-10-240-453-131	Sequence 131, App
c	23	23	1.2	8913	8	US-10-473-126-357	Sequence 357, App
	24	20	1.1	540	9	US-10-867-578-1	Sequence 1, Appli
	25	20	1.1	1612	7	US-10-424-599-90028	Sequence 90028, A
	26	20	1.1	50657	7	US-10-322-281-601	Sequence 601, App
c	27	20	1.1	135638	6	US-10-314-657-1	Sequence 1, Appli
c	28	20	1.1	135638	9	US-10-473-193-1	Sequence 1, Appli
c	29	19	1.0	300	9	US-10-779-543-7139	Sequence 7139, Ap
c	30	19	1.0	409	3	US-09-918-995-7331	Sequence 7331, Ap
c	31	19	1.0	486	8	US-10-425-115-66112	Sequence 66112, A
c	32	19	1.0	508	3	US-09-918-995-32346	Sequence 32346, A
c	33	19	1.0	512	3	US-09-918-995-32838	Sequence 32838, A
	34	19	1.0	531	4	US-09-925-065A-605191	Sequence 605191,
	35	19	1.0	538	6	US-10-369-493-30137	Sequence 30137, A
	36	19	1.0	583	7	US-10-021-323-5898	Sequence 5898, Ap
c	37	19	1.0	587	4	US-09-925-065A-821872	Sequence 821872,
	38	19	1.0	594	5	US-10-027-632-285111	Sequence 285111,
	39	19	1.0	594	5	US-10-027-632-285112	Sequence 285112,
	40	19	1.0	594	6	US-10-027-632-285111	Sequence 285111,
	41	19	1.0	594	6	US-10-027-632-285112	Sequence 285112,
	42	19	1.0	600	9	US-10-972-079-61446	Sequence 61446, A
	43	19	1.0	600	9	US-10-972-079-61447	Sequence 61447, A
	44	19	1.0	603	4	US-09-925-065A-605190	Sequence 605190,
c	45	19	1.0	607	5	US-10-027-632-94076	Sequence 94076, A

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 21:44:05 ; Search time 365.303 Seconds
                                        (without alignments)
                                        1576.107 Million cell updates/sec

Title: US-10-031-067A-8
Perfect score: 1850
Sequence: 1 ctcgaggatccagagacggc..........tctgtattaccatacggggg 1850

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 3289935 seqs, 155610033 residues

Word size :   0

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
                10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	1.0	2186	6	US-10-750-185-36969	Sequence 36969, A
c 2	18	1.0	1010	6	US-10-750-185-32271	Sequence 32271, A
c 3	18	1.0	1474	6	US-10-750-185-61406	Sequence 61406, A
4	18	1.0	1513	6	US-10-750-185-45456	Sequence 45456, A
5	18	1.0	1645	7	US-11-112-908-412	Sequence 412, App
6	18	1.0	2233	6	US-10-750-185-52967	Sequence 52967, A
7	18	1.0	2268	6	US-10-750-185-43837	Sequence 43837, A
8	18	1.0	3576	7	US-11-108-528-13	Sequence 13, Appl
9	18	1.0	161994	7	US-11-112-908-57	Sequence 57, Appl
10	18	1.0	168656	7	US-11-112-908-59	Sequence 59, Appl
11	18	1.0	170285	7	US-11-112-908-58	Sequence 58, Appl
12	17	0.9	19	8	US-11-101-244-86493	Sequence 86493, A
13	17	0.9	19	9	US-11-083-784-86493	Sequence 86493, A
14	17	0.9	837	6	US-10-793-626-2699	Sequence 2699, Ap

	15	17	0.9	941	6	US-10-750-185-51868	Sequence 51868, A
c	16	17	0.9	1049	6	US-10-750-185-64531	Sequence 64531, A
c	17	17	0.9	1327	6	US-10-750-185-26397	Sequence 26397, A
	18	17	0.9	1469	6	US-10-750-185-64406	Sequence 64406, A
	19	17	0.9	1604	6	US-10-750-185-56923	Sequence 56923, A
c	20	17	0.9	1635	6	US-10-793-626-37	Sequence 37, Appl
c	21	17	0.9	1729	6	US-10-750-185-64537	Sequence 64537, A
	22	17	0.9	1861	6	US-10-750-185-43369	Sequence 43369, A
	23	17	0.9	1873	6	US-10-750-185-47544	Sequence 47544, A
	24	17	0.9	2961	6	US-10-793-626-3347	Sequence 3347, Ap
	25	17	0.9	3236	6	US-10-793-626-3492	Sequence 3492, Ap
c	26	17	0.9	3459	6	US-10-793-626-3553	Sequence 3553, Ap
c	27	17	0.9	3487	6	US-10-750-185-48264	Sequence 48264, A
c	28	17	0.9	4420	6	US-10-131-826A-411	Sequence 411, App
c	29	16	0.9	408	7	US-11-112-908-403	Sequence 403, App
	30	16	0.9	549	7	US-11-108-172-497	Sequence 497, App
c	31	16	0.9	598	6	US-10-750-185-3880	Sequence 3880, Ap
	32	16	0.9	600	6	US-10-750-185-2700	Sequence 2700, Ap
c	33	16	0.9	600	6	US-10-750-185-3196	Sequence 3196, Ap
	34	16	0.9	600	6	US-10-750-185-4441	Sequence 4441, Ap
c	35	16	0.9	735	6	US-10-750-185-24628	Sequence 24628, A
	36	16	0.9	736	6	US-10-750-185-54269	Sequence 54269, A
c	37	16	0.9	747	6	US-10-067-974-5	Sequence 5, Appli
	38	16	0.9	774	6	US-10-750-185-61635	Sequence 61635, A
c	39	16	0.9	774	7	US-11-055-822-315	Sequence 315, App
c	40	16	0.9	781	7	US-11-112-908-332	Sequence 332, App
c	41	16	0.9	797	6	US-10-750-185-56736	Sequence 56736, A
	42	16	0.9	822	6	US-10-750-185-59347	Sequence 59347, A
c	43	16	0.9	831	6	US-10-821-234-649	Sequence 649, App
	44	16	0.9	844	6	US-10-750-185-58515	Sequence 58515, A
	45	16	0.9	847	6	US-10-750-185-32776	Sequence 32776, A

OM nucleic - nucleic search, using sw model

Run on: ·   December 5, 2005, 19:59:20 ; Search time 7106.02 Seconds
                                    (without alignments)
                                    12180.676 Million cell updates/sec

Title: US-10-031-067A-8
Perfect score: 1850
Sequence: 1 ctcgaggatccagagacggc.........tctgtattaccatacgggggg 1850

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size :   0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_est3:*
                4: gb_htc:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_est7:*
                9: gb_gss1:*
                10: gb_gss2:*
                11: gb_gss3:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	23	1.2	486	6	CA800611	CA800611 sau19a04.
2	22	1.2	299	2	BB445651	BB445651 BB445651
3	22	1.2	362	5	BY233275	BY233275 BY233275
4	22	1.2	831	11	CR835814	CR835814 GR0AAA7CH
5	22	1.2	884	11	CR835348	CR835348 GR0AAA7AD
6	21	1.1	393	1	AJ758173	AJ758173 AJ758173
7	21	1.1	439	9	AZ637045	AZ637045 1M0496D22
· 8	21	1.1	453	9	BZ160605	BZ160605 CH230-376
c 9	21	1.1	472	9	AZ840148	AZ840148 2M0136M03
c 10	21	1.1	505	11	CR817963	CR817963 GR0AAA43C
11	21	1.1	565	3	BI960934	BI960934 MONO1_2_G
c 12	21	1.1	640	8	CX356483	CX356483 ssalrgb52
13	21	1.1	652	10	CL584343	CL584343 OB__Ba007

c	14	21	1.1	689	8	CX356071		CX356071 ssalrgb55
c	15	21	1.1	726	9	CC948165		CC948165 BOIFY89TR
	16	21	1.1	767	10	AG134374		AG134374 Pan trogl
	17	21	1.1	836	9	BZ210963		BZ210963 CH230-280
	18	21	1.1	892	5	BQ428178		BQ428178 AGENCOURT
	19	20	1.1	158	8	N41309		N41309 yw68b08.r1
	20	20	1.1	215	7	CJ006639		CJ006639 CJ006639
c	21	20	1.1	232	5	BQ466966		BQ466966 HS02C08r
	22	20	1.1	251	10	CL436284		CL436284 PST2655-N
c	23	20	1.1	258	5	BQ466644		BQ466644 HS01C08T
c	24	20	1.1	321	11	DE093602		DE093602 Oryzias l
	25	20	1.1	352	1	AA016439		AA016439 mh37d01.r
	26	20	1.1	417	1	AA014858		AA014858 mh28e11.r
	27	20	1.1	443	3	BI673912		BI673912 ft30g11.y
c	28	20	1.1	445	2	BB676788		BB676788 BB676788
	29	20	1.1	448	1	AW485405		AW485405 65456 MAR
c	30	20	1.1	449	1	AL383286		AL383286 MtBC13B12
c	31	20	1.1	452	2	BB825187		BB825187 BB825187
c	32	20	1.1	454	2	BB785921		BB785921 BB785921
c	33	20	1.1	468	7	CN326691		CN326691 AGENCOURT
c	34	20	1.1	479	3	BI673693		BI673693 ft30g11.x
c	35	20	1.1	482	1	AI957805		AI957805 fd06b10.x
	36	20	1.1	491	1	AI508205		AI508205 mh37d01.y
	37	20	1.1	500	6	CD605506		CD605506 RK053A1H1
c	38	20	1.1	512	1	AL383287		AL383287 MtBC13B12
	39	20	1.1	520	5	BX525727		BX525727 BX525727
c	40	20	1.1	527	1	AW280000		AW280000 fj48a11.x
c	41	20	1.1	530	1	AW154144		AW154144 fi23b05.x
c	42	20	1.1	540	3	BQ131855		BQ131855 fz43c08.y
	43	20	1.1	546	1	AW072040		AW072040 ws58d06.x
c	44	20	1.1	546	3	BM778190		BM778190 fy29c04.x
c	45	20	1.1	565	1	AJ503079		AJ503079 AJ503079

Untitled

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 19:55:40 ; Search time 1391.77 Seconds
                                             (without alignments)
                                             11313.373 Million cell updates/sec

Title: US-10-031-067A-9
Perfect score: 277
Sequence: 1 ttctgcatctatggagtata..........tcctccacaggacagtgatc 277

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size :   0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_in:*
                 3: gb_env:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pr:*
                 9: gb_ro:*
                 10: gb_sts:*
                 11: gb_sy:*
                 12: gb_un:*
                 13: gb_vi:*
                 14: gb_htg:*
                 15: gb_pl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	277	100.0	277	6	AX079248	AX079248 Sequence
	2	277	100.0	1850	6	AX079247	AX079247 Sequence
	3	277	100.0	1850	6	AX079256	AX079256 Sequence
	4	181	65.3	2500	8	AF233371	AF233371 Homo sapi
	5	167	60.3	738	10	BV606780	BV606780 S216P6146
c	6	167	60.3	8913	6	AX598719	AX598719 Sequence
c	7	167	60.3	11913	6	CQ787205	CQ787205 Sequence
c	8	167	60.3	11913	6	CQ806558	CQ806558 Sequence

Page 1

c	9	167	60.3	11913	6	AX795666	AX795666 Sequence
c	10	167	60.3	11913	6	AX822117	AX822117 Sequence
c	11	167	60.3	11913	6	AX825757	AX825757 Sequence
c	12	167	60.3	50678	8	AY245105	AY245105 Homo sapi
c	13	167	60.3	127580	8	HSDJ74J1	AL049692 Human DNA
c	14	167	60.3	248214	14	AL138811	AL138811 Homo sapi
c	15	23	8.3	8170	6	AX323643	AX323643 Sequence
	16	20	7.2	534	15	AB180352	AB180352 Exobasidi
	17	20	7.2	536	15	AB180347	AB180347 Exobasidi
	18	20	7.2	536	15	AB180350	AB180350 Exobasidi
	19	20	7.2	536	15	AB180372	AB180372 Exobasidi
	20	20	7.2	539	15	AB180367	AB180367 Exobasidi
	21	20	7.2	544	15	AB180354	AB180354 Exobasidi
	22	20	7.2	552	15	AB180353	AB180353 Exobasidi
	23	20	7.2	552	15	AB180362	AB180362 Exobasidi
	24	20	7.2	597	15	BSU65624	U65624 Basidiomyce
	25	20	7.2	2765	5	BC056554	BC056554 Danio rer
	26	20	7.2	3490	5	DRU84616	U84616 Danio rerio
c	27	20	7.2	81296	14	AC165662	AC165662 Bos tauru
	28	20	7.2	110000	15	AP008217_027	Continuation (28 o
c	29	20	7.2	127338	15	AC134048	AC134048 Oryza sat
	30	20	7.2	147624	14	AC126056	AC126056 Oryza sat
	31	20	7.2	159632	15	AC133217	AC133217 Oryza sat
	32	20	7.2	176889	9	AC124830	AC124830 Mus muscu
c	33	20	7.2	191183	5	BX511211	BX511211 Zebrafish
	34	20	7.2	228120	5	CR388002	CR388002 Zebrafish
c	35	20	7.2	230932	14	AC116053	AC116053 Rattus no
	36	20	7.2	246455	14	AC130015	AC130015 Rattus no
	37	20	7.2	256444	14	AC109969	AC109969 Rattus no
c	38	20	7.2	286283	9	AC139214	AC139214 Mus muscu
	39	19	6.9	449	10	BV313600	BV313600 S236P635F
c	40	19	6.9	1256	8	AB209466	AB209466 Homo sapi
c	41	19	6.9	1629	8	BC089401	BC089401 Homo sapi
c	42	19	6.9	2078	6	AX833823	AX833823 Sequence
c	43	19	6.9	2078	8	AK095878	AK095878 Homo sapi
c	44	19	6.9	2225	8	BC037850	BC037850 Homo sapi
c	45	19	6.9	2530	8	HSM804062	AL832751 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:08:34 ; Search time 163.7 Seconds
                                              (without alignments)
                                              11277.487 Million cell updates/sec

Title: US-10-031-067A-9
Perfect score: 277
Sequence: 1 ttctgcatctatggagtata..........tcctccacaggacagtgatc 277

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size :   0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_21:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*
                14: geneseqn2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	277	100.0	277	4	AAD02662	Aad02662 Human WT1
2	277	100.0	1850	4	AAD02661	Aad02661 Human Wil
c 3	167	60.3	8913	8	ABZ09919	Abz09919 Human 5'
c 4	167	60.3	11913	10	ADB53953	Adb53953 WT1 genom
c 5	167	60.3	11913	13	ADS88992	Ads88992 Human WT1
c 6	23	8.3	8170	6	ABK28257	Abk28257 DNA trans
c 7	19	6.9	405	4	AAK57023	Aak57023 Human imm
c 8	19	6.9	508	9	ACH45134	Ach45134 Human foe
c 9	19	6.9	512	9	ACH45626	Ach45626 Human foe
10	19	6.9	583	13	ACN51117	Acn51117 Cotton an

	11	19	6.9	1470	2	AAT43943	Aat43943 Sequence
	12	19	6.9	1470	2	AAT72063	Aat72063 Sequence
c	13	19	6.9	1506	10	ADC30121	Adc30121 Human nov
c	14	19	6.9	2078	11	ADM02262	Adm02262 Human cDN
c	15	19	6.9	2885	13	ADR07390	Adr07390 Full leng
c	16	19	6.9	3451	10	ABZ79884	Abz79884 Human nuc
c	17	19	6.9	6173	4	AAS30504	Aas30504 DNA encod
c	18	19	6.9	6173	4	AAK69343	Aak69343 Human imm
c	19	19	6.9	6173	4	AAL06284	Aal06284 Human rep
c	20	19	6.9	6174	4	AAS30503	Aas30503 DNA encod
c	21	19	6.9	6174	4	AAK69342	Aak69342 Human imm
c	22	19	6.9	6174	4	AAL06283	Aal06283 Human rep
c	23	19	6.9	8743	2	AAV99284	Aav99284 Rupestris
c	24	19	6.9	9238	6	ABK28365	Abk28365 DNA trans
c	25	18	6.5	5921	4	AAS46655	Aas46655 Tumour su
c	26	18	6.5	5921	6	ABL33360	Abl33360 Human imm
c	27	18	6.5	29871	6	ABN86359	Abn86359 L. lactis
	28	18	6.5	76846	11	ACN44380	Acn44380 Mouse gen
c	29	18	6.5	110000	12	ADO34927_2	Continuation (3 of
c	30	17	6.1	165	13	ADS02236	Ads02236 Staphyloc
c	31	17	6.1	191	3	AAC07202	Aac07202 Human sec
c	32	17	6.1	202	9	ABX94314	Abx94314 Human bre
c	33	17	6.1	261	9	ABX94313	Abx94313 Human bre
c	34	17	6.1	286	9	ABX94312	Abx94312 Human bre
c	35	17	6.1	402	10	ADC32285	Adc32285 Human nov
	36	17	6.1	442	12	ADP92575	Adp92575 Cotton ex
c	37	17	6.1	573	13	ADQ52106	Adq52106 Novel can
c	38	17	6.1	578	12	ACH71434	Ach71434 Human gen
c	39	17	6.1	678	6	ABN69374	Abn69374 Streptoco
c	40	17	6.1	681	13	ADV84240	Adv84240 Streptoco
	41	17	6.1	837	4	AAH53653	Aah53653 S. epider
c	42	17	6.1	838	10	ADC30423	Adc30423 Human nov
c	43	17	6.1	1372	10	ADA13380	Ada13380 Human int
c	44	17	6.1	1716	3	AAZ35858	Aaz35858 Human cho
	45	17	6.1	1907	5	ABX71411	Abx71411 Human tes

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 21:06:40 ; Search time 54.4363 Seconds
                                              (without alignments)
                                              9045.152 Million cell updates/sec

Title: US-10-031-067A-9
Perfect score: 277
Sequence: 1 ttctgcatctatggagtata..........tcctccacaggacagtgatc 277

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                        %
Result   Query
   NO.   Score   Match Length DB ID   Description
----
 c   1   167   60.3   51754   3   US-09-949-016-15009   Sequence 15009, A
 c   2   167   60.3   51754   3   US-09-949-016-15010   Sequence 15010, A
 c   3   167   60.3   51754   3   US-09-949-016-15011   Sequence 15011, A
 c   4   167   60.3   51754   3   US-09-949-016-15012   Sequence 15012, A
 c   5   167   60.3   51754   3   US-09-949-016-15275   Sequence 15275, A
 c   6   167   60.3   51754   3   US-09-949-016-15276   Sequence 15276, A
 c   7   167   60.3   51754   3   US-09-949-016-15277   Sequence 15277, A
 c   8   167   60.3   51754   3   US-09-949-016-15278   Sequence 15278, A
     9   19   6.9   1470   2   US-08-599-252-97   Sequence 97, Appl
    10   19   6.9   1470   6   PCT-US96-06352-97   Sequence 97, Appl
    11   19   6.9   1470   6   PCT-US96-06583-97   Sequence 97, Appl
 c 12   19   6.9   6485   3   US-09-081-320-2   Sequence 2, Appli
 c 13   19   6.9   6485   3   US-09-574-141A-2   Sequence 2, Appli
 c 14   19   6.9   6485   3   US-09-707-780-2   Sequence 2, Appli
 c 15   19   6.9   6485   3   US-09-568-189A-2   Sequence 2, Appli

c	16	19	6.9	8743	3	US-09-081-320-1	Sequence 1, Appli
c	17	19	6.9	8743	3	US-09-574-141A-1	Sequence 1, Appli
c	18	19	6.9	8743	3	US-09-707-780-1	Sequence 1, Appli
c	19	19	6.9	8743	3	US-09-568-189A-1	Sequence 1, Appli
c	20	18	6.5	678533	3	US-09-949-016-14577	Sequence 14577, A
c	21	18	6.5	678533	3	US-09-949-016-14578	Sequence 14578, A
c	22	17	6.1	191	3	US-09-513-999C-11277	Sequence 11277, A
	23	17	6.1	400	3	US-09-270-767-8018	Sequence 8018, Ap
	24	17	6.1	400	3	US-09-270-767-23300	Sequence 23300, A
	25	17	6.1	837	3	US-09-710-279-2699	Sequence 2699, Ap
c	26	17	6.1	1716	2	US-08-954-333-9	Sequence 9, Appli
	27	17	6.1	2793	3	US-09-134-001C-2477	Sequence 2477, Ap
	28	17	6.1	2942	3	US-10-104-047-1534	Sequence 1534, Ap
	29	17	6.1	2976	3	US-09-386-962C-7	Sequence 7, Appli
	30	17	6.1	2976	3	US-09-386-959-7	Sequence 7, Appli
	31	17	6.1	3236	3	US-09-710-279-3492	Sequence 3492, Ap
c	32	17	6.1	3459	3	US-09-710-279-3553	Sequence 3553, Ap
	33	17	6.1	3600	3	US-09-147-405B-14	Sequence 14, Appl
c	34	17	6.1	4420	3	US-09-991-181-123	Sequence 123, App
c	35	17	6.1	4420	3	US-09-990-444-123	Sequence 123, App
c	36	17	6.1	4420	3	US-09-997-333-123	Sequence 123, App
c	37	17	6.1	4420	3	US-09-992-598-123	Sequence 123, App
c	38	17	6.1	4430	2	US-08-918-914-2	Sequence 2, Appli
c	39	17	6.1	5484	3	US-09-632-580A-3	Sequence 3, Appli
c	40	17	6.1	5501	2	US-08-484-438-1	Sequence 1, Appli
c	41	17	6.1	5555	2	US-08-484-438-3	Sequence 3, Appli
	42	17	6.1	58361	3	US-09-949-016-16755	Sequence 16755, A
	43	17	6.1	58361	3	US-09-949-016-16756	Sequence 16756, A
	44	17	6.1	59065	3	US-09-813-817-3	Sequence 3, Appli
	45	17	6.1	59065	3	US-09-978-197-3	Sequence 3, Appli

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 21:22:58 ; Search time 225.689 Seconds
                                            (without alignments)
                                            10149.433 Million cell updates/sec

Title: US-10-031-067A-9
Perfect score: 277
Sequence: 1 ttctgcatctatggagtata.........tcctccacaggacagtgatc 277

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size :   0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
                1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	167	60.3	8913	8	US-10-473-126-59	Sequence 59, Appl
c 2	23	8.3	8170	6	US-10-240-453-131	Sequence 131, App
3	20	7.2	1612	7	US-10-424-599-90028	Sequence 90028, A
c 4	19	6.9	508	3	US-09-918-995-32346	Sequence 32346, A
c 5	19	6.9	512	3	US-09-918-995-32838	Sequence 32838, A
6	19	6.9	583	7	US-10-021-323-5898	Sequence 5898, Ap
7	19	6.9	594	5	US-10-027-632-285111	Sequence 285111,
8	19	6.9	594	5	US-10-027-632-285112	Sequence 285112,
9	19	6.9	594	6	US-10-027-632-285111	Sequence 285111,
10	19	6.9	594	6	US-10-027-632-285112	Sequence 285112,
c 11	19	6.9	2078	6	US-10-108-260A-947	Sequence 947, App
c 12	19	6.9	3451	9	US-10-486-977-45	Sequence 45, Appl
c 13	19	6.9	6173	3	US-09-764-891-8972	Sequence 8972, Ap
c 14	19	6.9	6174	3	US-09-764-891-8971	Sequence 8971, Ap

c	15	19	6.9	6485	8	US-10-803-063-2	Sequence 2, Appli
c	16	19	6.9	8743	8	US-10-803-063-1	Sequence 1, Appli
c	17	19	6.9	9238	6	US-10-240-453-239	Sequence 239, App
c	18	18	6.5	308	4	US-09-925-065A-630148	Sequence 630148,
c	19	18	6.5	402	10	US-11-029-984-679	Sequence 679, App
	20	18	6.5	559	4	US-09-925-065A-109311	Sequence 109311,
	21	18	6.5	597	4	US-09-925-065A-573513	Sequence 573513,
	22	18	6.5	623	4	US-09-925-065A-152837	Sequence 152837,
c	23	18	6.5	636	4	US-09-925-065A-441670	Sequence 441670,
	24	18	6.5	954	5	US-10-027-632-149092	Sequence 149092,
	25	18	6.5	954	6	US-10-027-632-149092	Sequence 149092,
	26	18	6.5	1250	7	US-10-424-599-68178	Sequence 68178, A
c	27	18	6.5	5921	6	US-10-311-455-1333	Sequence 1333, Ap
c	28	18	6.5	5921	7	US-10-221-714A-377	Sequence 377, App
	29	18	6.5	76846	5	US-10-087-192-799	Sequence 799, App
c	30	18	6.5	382256	9	US-10-820-226-1	Sequence 1, Appli
c	31	18	6.5	382259	10	US-11-029-984-1	Sequence 1, Appli
c	32	18	6.5	3673778	6	US-10-312-841-2	Sequence 2, Appli
	33	17	6.1	25	8	US-10-719-900-213271	Sequence 213271,
c	34	17	6.1	165	7	US-10-724-972A-1531	Sequence 1531, Ap
c	35	17	6.1	202	3	US-09-104-408-9	Sequence 9, Appli
	36	17	6.1	219	7	US-10-437-963-95858	Sequence 95858, A
c	37	17	6.1	247	7	US-10-437-963-99061	Sequence 99061, A
c	38	17	6.1	261	3	US-09-104-408-8	Sequence 8, Appli
c	39	17	6.1	286	3	US-09-104-408-7	Sequence 7, Appli
	40	17	6.1	289	8	US-10-425-115-151835	Sequence 151835,
c	41	17	6.1	328	8	US-10-425-115-113603	Sequence 113603,
	42	17	6.1	442	3	US-09-732-627A-1586	Sequence 1586, Ap
	43	17	6.1	473	5	US-10-027-632-59954	Sequence 59954, A
	44	17	6.1	473	5	US-10-027-632-174418	Sequence 174418,
	45	17	6.1	473	6	US-10-027-632-59954	Sequence 59954, A

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 21:44:05 ; Search time 54.6968 Seconds
                                               (without alignments)
                                               1576.107 Million cell updates/sec

Title: US-10-031-067A-9
Perfect score: 277
Sequence: 1 ttctgcatctatggagtata..........tcctccacaggacagtgatc 277

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 3289935 seqs, 155610033 residues

Word size :   0

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                 1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
                 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	17	6.1	837	6	US-10-793-626-2699	Sequence 2699, Ap
c	2	17	6.1	1049	6	US-10-750-185-64531	Sequence 64531, A
	3	17	6.1	3236	6	US-10-793-626-3492	Sequence 3492, Ap
c	4	17	6.1	3459	6	US-10-793-626-3553	Sequence 3553, Ap
c	5	17	6.1	4420	6	US-10-131-826A-411	Sequence 411, App
c	6	16	5.8	747	6	US-10-067-974-5	Sequence 5, Appli
c	7	16	5.8	797	6	US-10-750-185-56736	Sequence 56736, A
c	8	16	5.8	867	7	US-11-055-822-35	Sequence 35, Appl
	9	16	5.8	954	6	US-10-674-767-1	Sequence 1, Appli
c	10	16	5.8	1129	6	US-10-750-185-34322	Sequence 34322, A
c	11	16	5.8	1410	6	US-10-750-185-54190	Sequence 54190, A
c	12	16	5.8	1440	6	US-10-750-185-37316	Sequence 37316, A
	13	16	5.8	1652	6	US-10-750-185-33809	Sequence 33809, A
c	14	16	5.8	1706	6	US-10-750-185-38413	Sequence 38413, A

	15	16	5.8	1741	6	US-10-750-185-26423	Sequence 26423, A
	16	16	5.8	1783	6	US-10-750-185-56643	Sequence 56643, A
c	17	16	5.8	1967	6	US-10-750-185-27677	Sequence 27677, A
c	18	16	5.8	2106	6	US-10-750-185-28928	Sequence 28928, A
c	19	16	5.8	2173	6	US-10-750-185-27026	Sequence 27026, A
c	20	16	5.8	2215	7	US-11-147-047-22	Sequence 22, Appl
	21	16	5.8	2342	6	US-10-750-185-40248	Sequence 40248, A
c	22	16	5.8	3213	7	US-11-147-047-23	Sequence 23, Appl
	23	16	5.8	10373	6	US-10-821-234-64	Sequence 64, Appl
	24	16	5.8	207600	7	US-11-112-908-31	Sequence 31, Appl
	25	15	5.4	19	8	US-11-101-244-842511	Sequence 842511,
	26	15	5.4	19	8	US-11-101-244-947156	Sequence 947156,
	27	15	5.4	19	8	US-11-101-244-947172	Sequence 947172,
	28	15	5.4	19	8	US-11-101-244-947250	Sequence 947250,
	29	15	5.4	19	8	US-11-101-244-947266	Sequence 947266,
	30	15	5.4	19	8	US-11-101-244-947350	Sequence 947350,
	31	15	5.4	19	8	US-11-101-244-947366	Sequence 947366,
	32	15	5.4	19	8	US-11-101-244-1189574	Sequence 1189574,
c	33	15	5.4	19	8	US-11-101-244-1229568	Sequence 1229568,
	34	15	5.4	19	9	US-11-083-784-842511	Sequence 842511,
	35	15	5.4	19	9	US-11-083-784-947156	Sequence 947156,
	36	15	5.4	19	9	US-11-083-784-947172	Sequence 947172,
	37	15	5.4	19	9	US-11-083-784-947250	Sequence 947250,
	38	15	5.4	19	9	US-11-083-784-947266	Sequence 947266,
	39	15	5.4	19	9	US-11-083-784-947350	Sequence 947350,
	40	15	5.4	19	9	US-11-083-784-947366	Sequence 947366,
	41	15	5.4	19	9	US-11-083-784-1189574	Sequence 1189574,
c	42	15	5.4	19	9	US-11-083-784-1229568	Sequence 1229568,
	43	15	5.4	695	6	US-10-750-185-32341	Sequence 32341, A
	44	15	5.4	724	7	US-11-055-822-293	Sequence 293, App
	45	15	5.4	741	6	US-10-750-185-56750	Sequence 56750, A

Untitled
GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 19:59:20 ; Search time 1063.98 Seconds
                                          (without alignments)
                                 12180.676 Million cell updates/sec

Title: US-10-031-067A-9
Perfect score: 277
Sequence: 1 ttctgcatctatggagtata..........tcctccacaggacagtgatc 277

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size :   0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_est3:*
                4: gb_htc:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_est7:*
                9: gb_gss1:*
                10: gb_gss2:*
                11: gb_gss3:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1   22   7.9   299   2   BB445651   BB445651 BB445651
      2   20   7.2   215   7   CJ006639   CJ006639 CJ006639
      3   20   7.2   352   1   AA016439   AA016439 mh37d01.r
      4   20   7.2   417   1   AA014858   AA014858 mh28e11.r
      5   20   7.2   443   3   BI673912   BI673912 ft30g11.y
  c   6   20   7.2   479   3   BI673693   BI673693 ft30g11.x
  c   7   20   7.2   482   1   AI957805   AI957805 fd06b10.x
      8   20   7.2   491   1   AI508205   AI508205 mh37d01.y
      9   20   7.2   520   5   BX525727   BX525727 BX525727
  c 10   20   7.2   527   1   AW280000   AW280000 fj48a11.x
  c 11   20   7.2   530   1   AW154144   AW154144 fi23b05.x
  c 12   20   7.2   540   3   BQ131855   BQ131855 fz43c08.y
  c 13   20   7.2   546   3   BM778190   BM778190 fy29c04.x
                                Page 1

	14	20	7.2	579	5	BU926825	BU926825 sas92b03.
c	15	20	7.2	600	1	AW595335	AW595335 fk30f08.y
	16	20	7.2	718	10	CL852188	CL852188 OR_CBa008
	17	20	7.2	765	7	CK027599	CK027599 AGENCOURT
	18	20	7.2	851	8	DR930354	DR930354 EST112189
c	19	20	7.2	868	11	HT7113I9	CR957493 Equus cab
c	20	20	7.2	903	7	CK706381	CK706381 ZF101-P00
c	21	20	7.2	921	5	BU455842	BU455842 603216810
c	22	20	7.2	986	10	CG876393	CG876393 ZMMBBc028
	23	19	6.9	255	2	BF741702	BF741702 CM4-HB002
c	24	19	6.9	259	2	BB598313	BB598313 BB598313
	25	19	6.9	285	10	CE267276	CE267276 tigr-gss-
	26	19	6.9	419	2	BB817765	BB817765 BB817765
c	27	19	6.9	452	1	AA432010	AA432010 zw80b10.r
	28	19	6.9	463	1	AI911852	AI911852 wc79b09.x
	29	19	6.9	468	8	N51619	N51619 yy98g07.s1
	30	19	6.9	476	1	AI376031	AI376031 ta57h01.x
c	31	19	6.9	485	6	CA391470 ·	CA391470 cs15f08.y
	32	19	6.9	553	1	AW118893	AW118893 xd98a03.x
	33	19	6.9	554	1	AA448473	AA448473 zw80b10.s
	34	19	6.9	583	2	BF061904	BF061904 7k68g02.x
	35	19	6.9	680	11	DE087987	DE087987 Oryzias l
c	36	19	6.9	682	8	DN956265	DN956265 Fh_mx0_16
	37	19	6.9	695	3	BM682010	BM682010 UI-E-EO1-
	38	19	6.9	712	6	CA435417	CA435417 UI-H-DT0-
	39	19	6.9	719	9	CE187187	CE187187 tigr-gss-
	40	19	6.9	747	10	BX169228	BX169228 Danio rer
c	41	19	6.9	773	2	BG764475	BG764475 602736509
	42	19	6.9	779	9	BH425168	BH425168 BOGVL42TF
c	43	19	6.9	844	7	CN990286	CN990286 66463_125
	44	19	6.9	992	2	BG389211	BG389211 602413846
c	45	19	6.9	1046	2	BE733351	BE733351 601570577